



REPLACEMENT SHEETS

Pea Chalcone reductase DNA sequence (SEQ ID No. 1)

```
1   ATGGGTTAGTG TTGAAATCCC AACAAAGGTG CTTACCAACA CATCTGCTCA AATTAAGATG
61  CCTGTTGTTG GAATGGGATC AGCACCTGAC TTCACATGCA AGAAAGACAC TAAAGAAGCA
121 ATCATCGAAG CCATCAAACA AGGTTACAGA CACTTTGATA CTGCTGCTGC TTATGGATCC
181 GAACAAGCTC TTGGTGAGGC TTTGAATGAG GCTATTCAAC TTGGTCTTGT CACTAGAGAA
241 CAGCTTTTGT TTA CTCTCTAA ACTTTGGGTT ACTGAAAATC ATCCTCACCT TGTTCCTCCT
301 GCTCTACAAA AATCTCTCAA GACTCTTCAG TTGGATTACT TGGATTTGTA TTTGATTCAT
361 TGGCCACTTA GTTCTCAGCC CGGAAAGTTT TCATTTCCAA TTGATGTGGC TGATCTATTG
421 CCATTTGATG TAAAGGTGT GTGGGAATCC ATGGAAGAGG CTTTGAGACT TGGACTCAGC
481 AAAGCTATTG GTGTCAGTAA CTTCTCTGTC AAGAAACTTC AAAAGCTACT ATCTGTTGCC
541 ACTGTTCTTC CTGCTGTTAA TCAAGTAGAG ATGAACCTTG CATGGCAACA AAAGAAGCTA
601 AGAGAATTTT GCAATGAAAA TGGAATAGTG TTGACTGCAT TTTCACCGTT GAGGAAAGGC
661 GCCAGCCGAG GAGCAAATGA GGTTATGGAG AATGATATGE TTAAACAGAT TGCAGATGCT
721 CATGGAAAGT CTATTGCACA AATTTCTCTG AGATGGTTAT ATGAACAAGG AATCACTTTT
781 GTTCCAAAGA GCTATGATAA GGAGAGAATG AGTCAAAATT TGAGAATCTT TGATTGGACA
841 CTGACAAAGG AGGATCATGA GAAAATTGAT CAAATTAAGC AGAATCGTTT GATCCCTGGA
901 CCAACCAAGC CAAGTCTCAA TGATCTTTGG GATGATGAAA TATAAG
```

Pea Chalcone reductase protein sequence (SEQ ID No. 2)

```
Met Gly Ser Val Glu Ile Pro Thr Lys Val Leu Thr Asn Thr Ser Ala Gln Ile Lys Met
Pro Val Val Gly Met Gly Ser Ala Pro Asp Phe Thr Cys Lys Lys Asp Thr Lys Glu Ala
Ile Ile Glu Ala Ile Lys Gln Gly Tyr Arg His Phe Asp Thr Ala Ala Ala Tyr Gly Ser
Glu Gln Ala Leu Gly Glu Ala Leu Asn Glu Ala Ile Gln Leu Gly Leu Val Thr Arg Glu
Gln Leu Phe Val Thr Ser Lys Leu Trp Val Thr Glu Asn His Pro His Leu Val Leu Pro
Ala Leu Gln Lys Ser Leu Lys Thr Leu Gln Leu Asp Tyr Leu Asp Leu Tyr Leu Ile His
Trp Pro Leu Ser Ser Gln Pro Gly Lys Phe Ser Phe Pro Ile Asp Val Ala Asp Leu Leu
Pro Phe Asp Val Lys Gly Val Trp Glu Ser Met Glu Glu Ala Leu Arg Leu Gly Leu Thr
Lys Ala Ile Gly Val Ser Asn Phe Ser Val Lys Lys Leu Gln Lys Leu Leu Ser Val Ala
Thr Val Leu Pro Ala Val Asn Gln Val Glu Met Asn Leu Ala Trp Gln Gln Lys Lys Leu
Arg Glu Phe Cys Asn Glu Asn Gly Ile Val Leu Thr Ala Phe Ser Pro Leu Arg Lys Gly
Ala Ser Arg Gly Ala Asn Glu Val Met Glu Asn Asp Met Leu Lys Gln Ile Ala Asp Ala
His Gly Lys Ser Ile Ala Gln Ile Ser Leu Arg Trp Leu Tyr Glu Gln Gly Ile Thr Phe
Val Pro Lys Ser Tyr Asp Lys Glu Arg Met Ser Gln Asn Leu Arg Ile Phe Asp Trp Thr
Leu Thr Lys Glu Asp His Glu Lys Ile Asp Gln Ile Lys Gln Asn Arg Leu Ile Pro Gly
Pro Thr Lys Pro Ser Leu Asn Asp Leu Trp Asp Asp Glu Ile
```

Fig. 1

REPLACEMENT SHEETS

Soy isoflavone synthase DNA sequence (SEQ ID No. 3)

```

1      ATGGTGCTTG AACTTGCACT TGGTTTATTG GTTTTGGCTC TGTTTCTGCA CTTGCGTCCC
61     ACACCCACTG CAAAATCAAA AGCACTTCGC CATCTCCCAA ACCCACCAAG CCCAAAGCCT
121    CGTCTTCCCT TCATAGGACA CCTTCATCTC TTAAGAGACA AACTTCTCCA CTACGCACTC
181    ATCGACCTCT CCAAAAAACA TGGTCCCTTA TTCTCTCTCT ACTTTGGCTC CATGCCAACC
241    GTTGTTCCTT CCACACCAGA ATTGTTCAAG CTCTTCCTCC AAACGCACGA GGCAACTTCC
301    TTCAACACAA GGTTCCAAAC CTCAGCCATA AGACGCCTCA CCTATGATAG CTCAGTGGCA
361    ATGGTTCCTT TCGGGCCCTA CTGGAAGTTC GTGAGGAAGC TCATCATGAA CGACCTTCTC
421    AACGCCACCA CTGTAAACAA GTTGAGGCCT TTGAGGACCC AACAGACGCG TAAGTTCCTT
481    AGGGTTATGG CCAAGGCGC AGAGGCACAG AAGCCCCTTG ACTTGACCGA GGAGCTTCTG
541    AAATGGACCA ACAGCACCAT CTCCATGATG ATGCTCGGCG AGGCTGAGGA GATCAGAGAC
601    ATCGCTCGCG AGGTTCTTAA GATCTTTGGC GAATACAGCC TCACTGACTT CATCTGGCCA
661    TTGAAGCATC TCAAGGTTGG AAAGTATGAG AAGAGGATCG ACGACATCTT GAACAAGTTC
721    GACCCTGTCTG TTGAAAGGGT CATCAAGAAG CGCCGTGAGA TCGTGAGGAG GAGAAAGAAC
781    GGAGAGGTTG TTGAGGGTGA GGTCAGCGGG GTTTTCCTTG ACACTTTGCT CGAGTTCGCT
841    GAGGATGAGA CTATGGAGAT CAAAATCACC AAGGACCACA TCAAGGGTCT TGTGTAGAC
901    TTTTCTCGG CAGGAACAGA CTCAACAGCG GTGGCAACAG AGTGGGCATT GGCAGAACTC
961    ATCAACAATC CTAAGGTGTT GGAAAAGGCT CGTGAGGAGG TCTACAGTGT TGTGGGAAAG
1021   GACAGACTTG TGGACGAAGT TGGCACTCAA AACCTTCCTT ACATTAGAGC AATCGTGAAG
1081   GAGACATTCC GCATGCACCC GCCACTCCCA GTGGTCAAAA GAAAGTGCAC AGAAGAGTGT
1141   GAGATTAATG GATATGTGAT CCCAGAGGGA GCATTGATTC TCTTCAATGT ATGGCAAGTA
1201   GGAAGAGACC CCAATACTG GGACAGACCA TCGGAGTTCC GTCCTGAGAG GTTCCTAGAG
1261   ACAGGGGCTG AAGGGGAAGC AGGGCCTCTT GATCTTAGGG GACAACATTT TCAACTTCTC
1321   CCATTTGGGT CTGGGAGGAG AATGTGCCCT GGAGTCAATC TGGCTACTTC GGGAAATGGCA
1381   ACACTTCTTG CATCTCTTAT TCAGTGCTTC GACTTGCAAG TGCTGGGTCC ACAAGGACAG
1441   ATATTGAAGG GTGGTGACGC CAAAGTTAGC ATGGAAGAGA GAGCCGGCCT CACTGTTCCT
1501   AGGGCACATA GTCTTGTCTG TGTCCACTT GCAAGGATCG GCCTTGCATC TAAACTCCTT
1561   TCTTAAG
  
```

Soy isoflavone synthase protein sequence (SEQ ID No. 4)

```

Met Val Leu Glu Leu Ala Leu Gly Leu Leu Val Leu Ala Leu Phe Leu His Leu
Arg Pro Thr Pro Thr Ala Lys Ser Lys Ala Leu Arg His Leu Pro Asn Pro Pro
Ser Pro Lys Pro Arg Leu Pro Phe Ile Gly His Leu His Leu Leu Lys Asp Lys
Leu Leu His Tyr Ala Leu Ile Asp Leu Ser Lys Lys His Gly Pro Leu Phe Ser
Leu Tyr Phe Gly Ser Met Pro Thr Val Val Ala Ser Thr Pro Glu Leu Phe Lys
Leu Phe Leu Gln Thr His Glu Ala Thr Ser Phe Asn Thr Arg Phe Gln Thr Ser
Ala Ile Arg Arg Leu Thr Tyr Asp Ser Ser Val Ala Met Val Pro Phe Gly Pro
Tyr Trp Lys Phe Val Arg Lys Leu Ile Met Asn Asp Leu Leu Asn Ala Thr Thr
Val Asn Lys Leu Arg Pro Leu Arg Thr Gln Gln Thr Arg Lys Phe Leu Arg Val
Met Ala Gln Gly Ala Glu Ala Gln Lys Pro Leu Asp Leu Thr Glu Glu Leu Leu
Lys Trp Thr Asn Ser Thr Ile Ser Met Met Met Leu Gly Glu Ala Glu Glu Ile
Arg Asp Ile Ala Arg Glu Val Leu Lys Ile Phe Gly Glu Tyr Ser Leu Thr Asp
Phe Ile Trp Pro Leu Lys His Leu Lys Val Gly Lys Tyr Glu Lys Arg Ile Asp
Asp Ile Leu Asn Lys Phe Asp Pro Val Val Glu Arg Val Ile Lys Lys Arg Arg
Glu Ile Val Arg Arg Arg Lys Asn Gly Glu Val Val Glu Gly Glu Val Ser Gly
Val Phe Leu Asp Thr Leu Leu Glu Phe Ala Glu Asp Glu Thr Met Glu Ile Lys
Ile Thr Lys Asp His Ile Lys Gly Leu Val Val Asp Phe Phe Ser Ala Gly Thr
Asp Ser Thr Ala Val Ala Thr Glu Trp Ala Leu Ala Glu Leu Ile Asn Asn Pro
Lys Val Leu Glu Lys Ala Arg Glu Glu Val Tyr Ser Val Val Gly Lys Asp Arg
Leu Val Asp Glu Val Asp Thr Gln Asn Leu Pro Tyr Ile Arg Ala Ile Val Lys
Glu Thr Phe Arg Met His Pro Pro Leu Pro Val Val Lys Arg Lys Cys Thr Glu
Glu Cys Glu Ile Asn Gly Tyr Val Ile Pro Glu Gly Ala Leu Ile Leu Phe Asn
Val Trp Gln Val Gly Arg Asp Pro Lys Tyr Trp Asp Arg Pro Ser Glu Phe Arg
Pro Glu Arg Phe Leu Glu Thr Gly Ala Glu Gly Glu Ala Gly Pro Leu Asp Leu
Arg Gly Gln His Phe Gln Leu Leu Pro Phe Gly Ser Gly Arg Arg Met Cys Pro
Gly Val Asn Leu Ala Thr Ser Gly Met Ala Thr Leu Leu Ala Ser Leu Ile Gln
Cys Phe Asp Leu Gln Val Leu Gly Pro Gln Gly Gln Ile Leu Lys Gly Gly Asp
Ala Lys Val Ser Met Glu Glu Arg Ala Gly Leu Thr Val Pro Arg Ala His Ser
Leu Val Cys Val Pro Leu Ala Arg Ile Gly Val Ala Ser Lys Leu Leu Ser
  
```

Fig. 2

REPLACEMENT SHEETS

Lotus corniculatus chalcone isomerase DNA sequence (SEQ ID No. 5)

```

1      ATGGCTGCAT CCCTCACCCC AATCCAGGTC GAGAACCTTC AATTCCTGC GTCTGTCACC
61     TCTCCAGCCA CCGCCAAGTC TTATTCCTC GGTGGTGAG GGGAGAGAGG GTTGACGATT
121    GAGGGGAAGT TCATAAAATT CACTGGCATA GGAGTGTATT TGGGAAGATAC AGCAGTGGAT
181    TCACTCGCCA CCAAGTGGAA GGGTAAGAGT TCACAAGAGC TGCAGGACTC CCTTGACTTC
241    TTCAGAGACA TCATTTCAAG TCCCTCTGAG AAGTTAATTC GAGGGTCCAA GCTGAGGCCA
301    TTGAGTGCGG TGGAGTATTC AAGAAAGGTG ATGGAGAATT GTGTGGCACA CATGAAGTCT
361    GCTGGAACTT ATGGTGAAGC AGAGGCCACA GCCATTGAAA AATTTCGAGA AGCCTTCAGG
421    AAGGTGGATT TTCCACCAGG TTCCTCTGTT TTCTACCGAC AATCAACAGA TGGAAAATTA
481    GGGCTTAGTT TCTCTTTGGA TGACACGATA CCAGAAGAAG AGGCTGTAGT TATAGAGAAC
541    AAGGCACTCT CAGAGGCAGT GTTAGAGACC ATGATTGGCG AGCATGCTGT TTCCCCTGAT
601    TTGAAGCGTT GTTTGGCTGA AAGGTTGCCT ATTGTGATGA ACCAGGGTCT TCTCCTCACT
661    GGAAACTGAT

```

Lotus corniculatus chalcone isomerase protein (SEQ ID No. 6)

```

Met Ala Ala Ser Leu Thr Pro Ile Gln Val Glu Asn Leu Gln Phe Pro Ala Ser
Val Thr Ser Pro Ala Thr Ala Lys Ser Tyr Phe Leu Gly Gly Ala Gly Glu Arg
Gly Leu Thr Ile Glu Gly Lys Phe Ile Lys Phe Thr Gly Ile Gly Val Tyr Leu
Glu Asp Thr Ala Val Asp Ser Leu Ala Thr Lys Trp Lys Gly Lys Ser Ser Gln
Glu Leu Gln Asp Ser Leu Asp Phe Phe Arg Asp Ile Ile Ser Ser Pro Ser Glu
Lys Leu Ile Arg Gly Ser Lys Leu Arg Pro Leu Ser Gly Val Glu Tyr Ser Arg
Lys Val Met Glu Asn Cys Val Ala His Met Lys Ser Ala Gly Thr Tyr Gly Glu
Ala Glu Ala Thr Ala Ile Glu Lys Phe Ala Glu Ala Phe Arg Lys Val Asp Phe
Pro Pro Gly Ser Ser Val Phe Tyr Arg Gln Ser Thr Asp Gly Lys Leu Gly Leu
Ser Phe Ser Leu Asp Asp Thr Ile Pro Glu Glu Glu Ala Val Val Ile Glu Asn
Lys Ala Leu Ser Glu Ala Val Leu Glu Thr Met Ile Gly Glu His Ala Val Ser
Pro Asp Leu Lys Arg Cys Leu Ala Glu Arg Leu Pro Ile Val Met Asn Gln Gly
Leu Leu Leu Thr Gly Asn

```

Fig. 3

REPLACEMENT SHEETS

ID No.	Primer	Primer Sequence (5' to 3')
13	GPTV1	Ttgtccagatagcccagtagctg
14	GPTV2	Cgacaatctgatcatgagcggag
15	30035S	Cgcaagacccttcctctatataag
16	Gus2	Gcatcacgcagttcaacgctg
17	152	Ggaaacagctatgaccatgattac
18	160	Aaggatccgtcgacatc
19	167	Agcccccatggtacgtcctgtagaaacc
20	168	Cgttttcgtcggtaatcaccattcc
21	191	Tttcccagtcacgacgttgt
22	198	Gacatcgataatacgac
23	248	Tgctacctctagagaatttccccg
24	321	ctaagcccc/taag/tattccatcaggtgatt
25	322	ccaggtggaaaatta/cacat/gt/gcttgaaa/gagc
26	323	tttgaaaagt/ctaataa/cgagggtca/gaag
27	324	tactcaaggaaggtt/gatggag/aactgt/cgtgg
28	329	cgcgagctcatgtacccccgggatttccactagtttaaggggttaactacatggtcgacgta cata
29	330	agcttatgtacgtcgaccatgtagtttaabcccttaactagtggaatccccgggggtacatg agctcgcgat
30	331	aattcgagctcatgtacccccgggatttccactagtttaaggggttaactacatggtcgacg
31	332	ctagcgtcgaccatgtagtttaacccttaactagtggaatccccgggggtacatgagctcg
32	333	catggatgcgtagtttaagcct
33	334	ctagaggccttacatacgcac
34	337	Aattcatgtacgagctcaattcccccgggataggcactagtgctgctgttaactacatgg tcgacttattaa
35	338	Aggtttaataagtcgaccatgtagtttaacagcagcactagtgcttatccccgggggaattg agctcgtacatg
36	339	Gaacacatgggtgcttgaacttgc
37	340	Tccagtagggccgaagggaaccattgccac
38	341	Ccttcggggccctactggaag
39	342	Cagcgaaactcgagcaaatg
40	343	Cactttgctcgagttcgctgaggatgagactatggagatcaaaatcaccaaggaccacat caagggctcttgtttagac
41	344	atgacgagctagcttattaagaaaggag
42	362	ggtgtgtggggatccatggaagaggctttg
43	363	cctcggctcgcgcttctcctcaacgggtgaaaatgcagtcacac
44	384	caacaacccatgggtagtggtgaaatcccaacaaagggtgcttacc
45	385	agcaactgctagcttatatttcacatcccaaagatc
46	386	tagattgccatggctgcacccctcaccccaatccaggtcgag
47	387	aaactttgctagcttatcagtttccagtgaggagaagac
48	398	gcttgttcggatccataagcagc
49	399	tgcttatggatccgaacaagctcttgggtgaggctttgaatg
50	400	cagccacatcaattggaaatg
51	401	tcatttccaattgatgtggctgatctattgccatttgatgtaaaagggtgtgtgggaatcc atggaagaggctttgaga
52	402	cacaagagctgcaggactcccttga
53	403	gggagtcctgcagctcttgtgaac
54	624	agctgcgatcgcaagcttggtagccgggaattctctaga
55	625	aatttctagagaattcccgtaccaagcttgcttgcgatcgc
56	626	tcgacctatggcccgtagccaattggagct
57	627	ccaattggctagcgggccatggg
58	640	ccaccacgagggaacatcgtg
59	641	gaattcccattggtttacactcgaggctcctctccaaatga

Fig. 4

Fig.5.

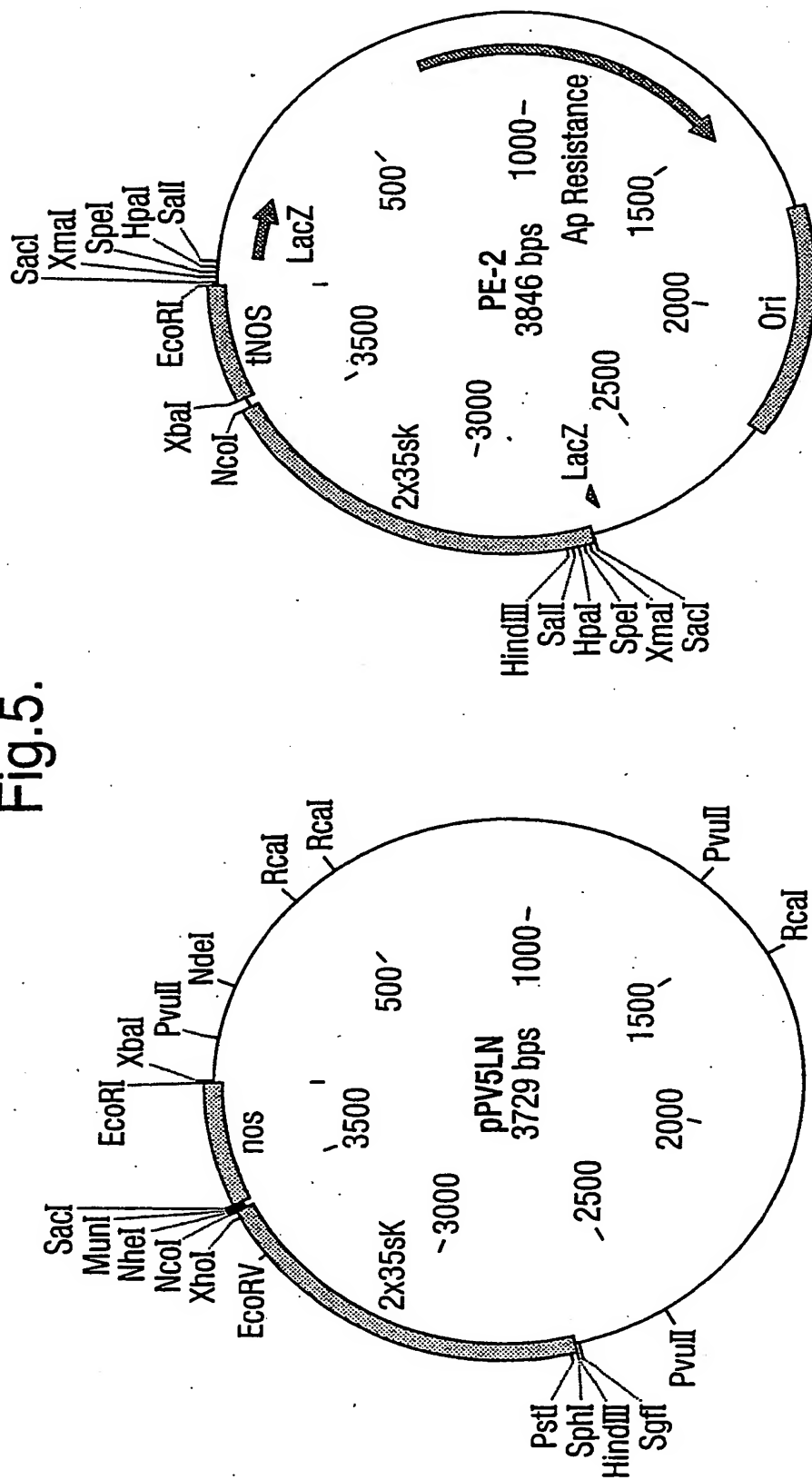


Fig.5 (Cont I).

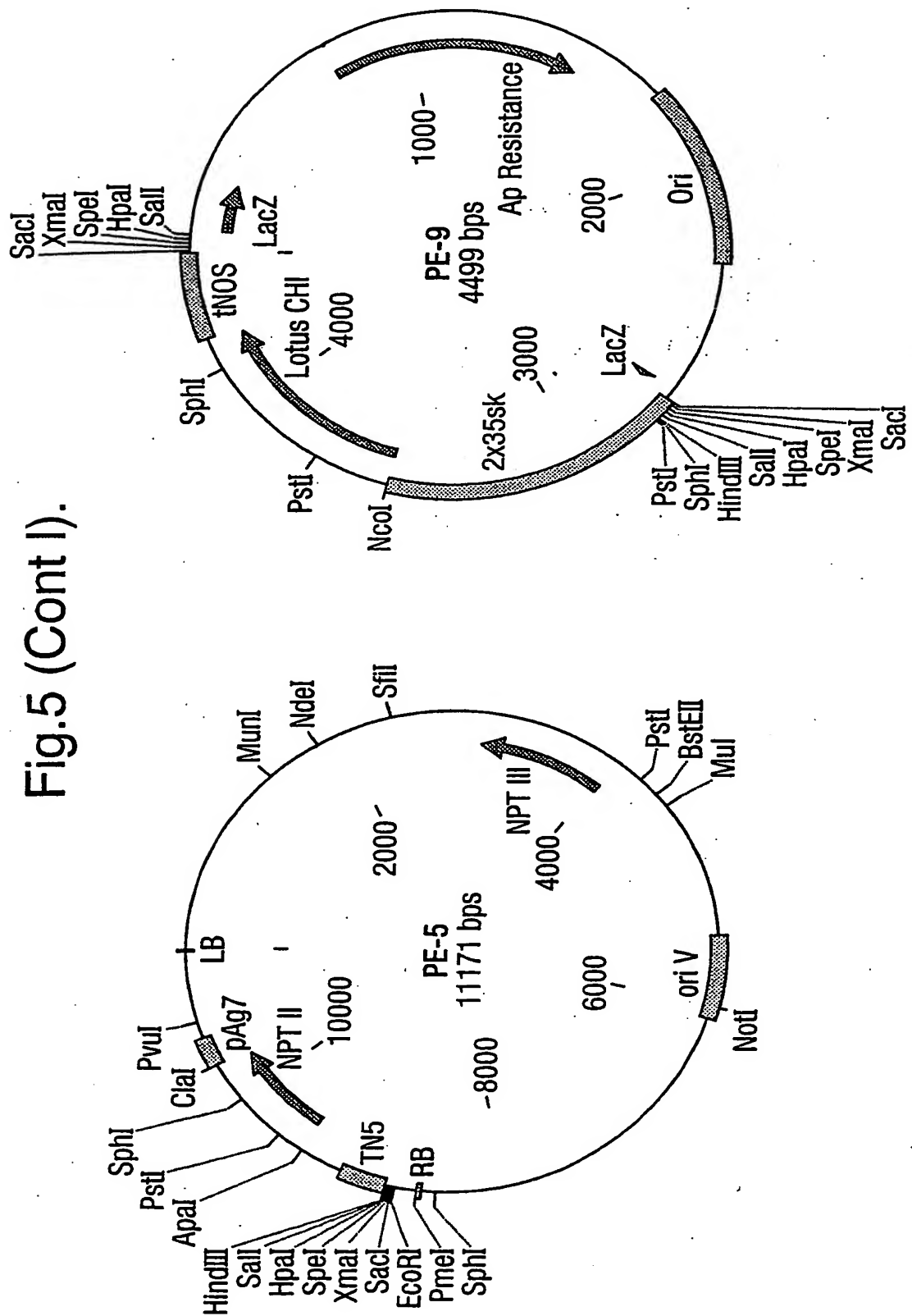
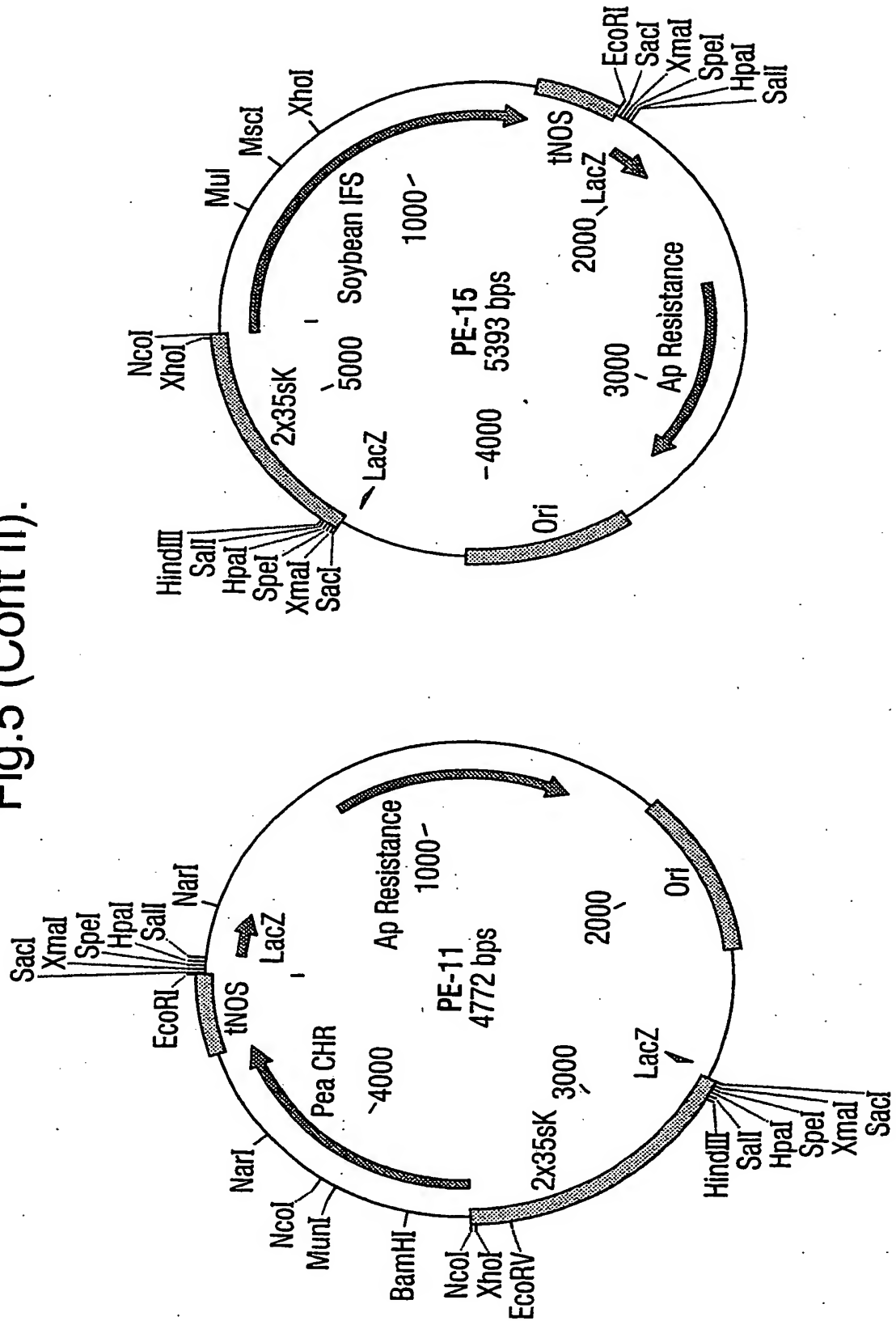


Fig.5 (Cont II).



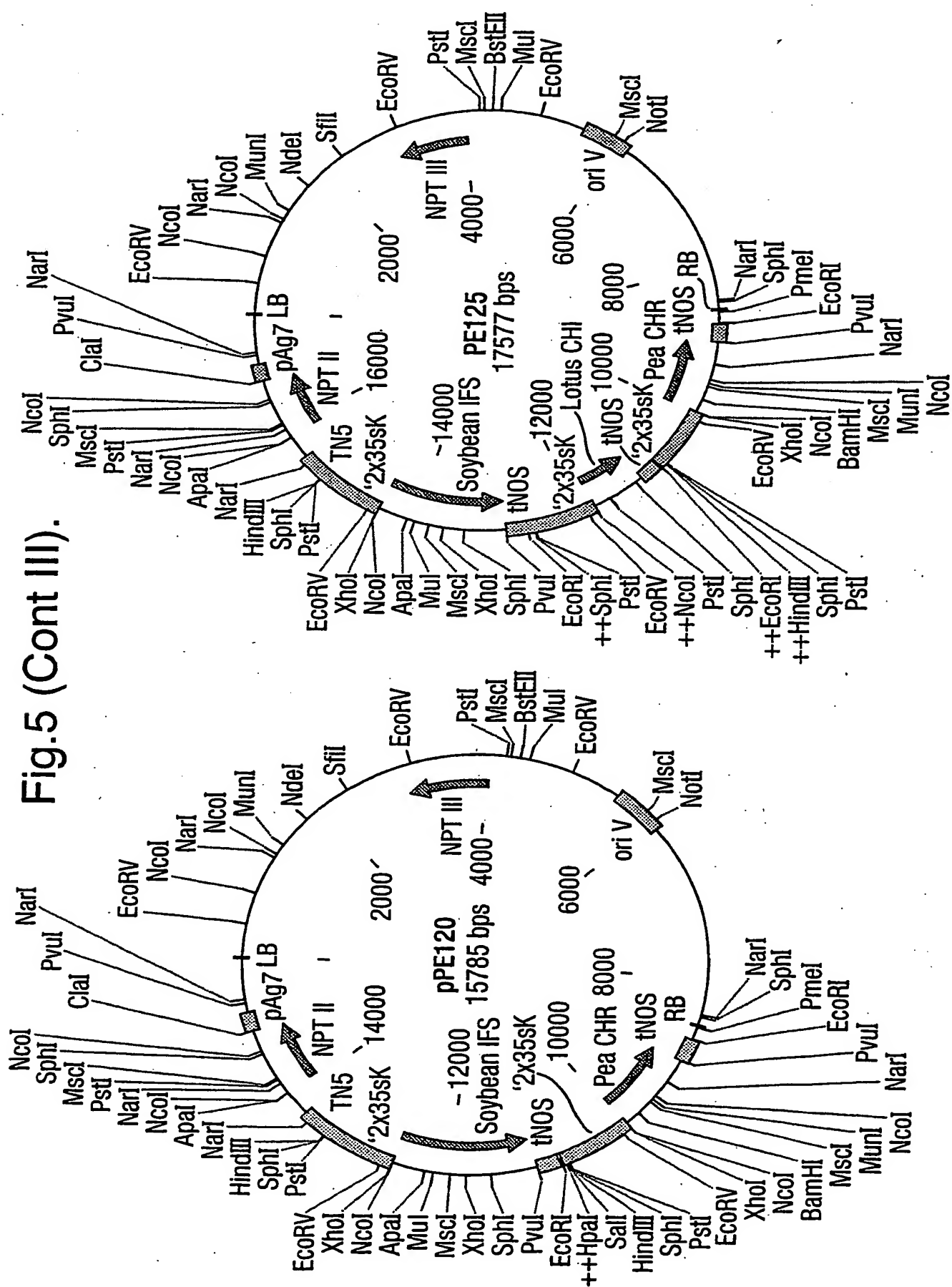


Fig.5 (Cont IIII).

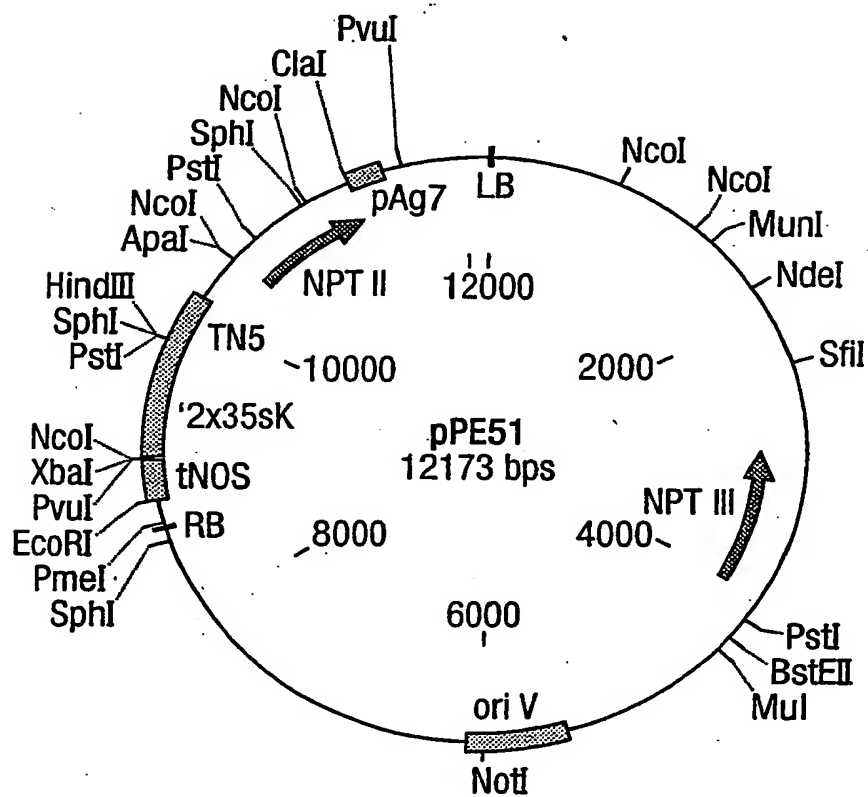


Fig.6a.

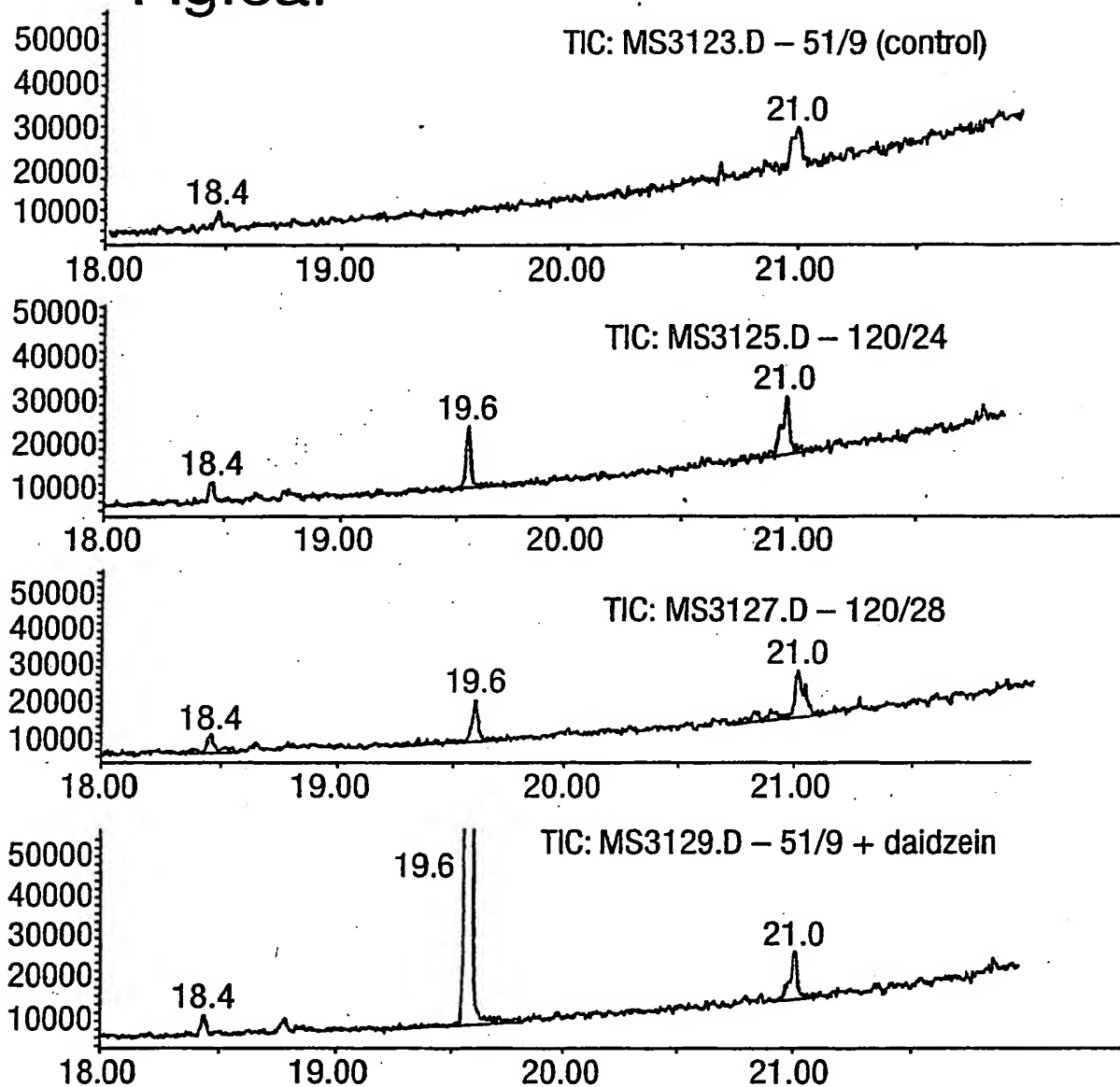


Fig.6b.

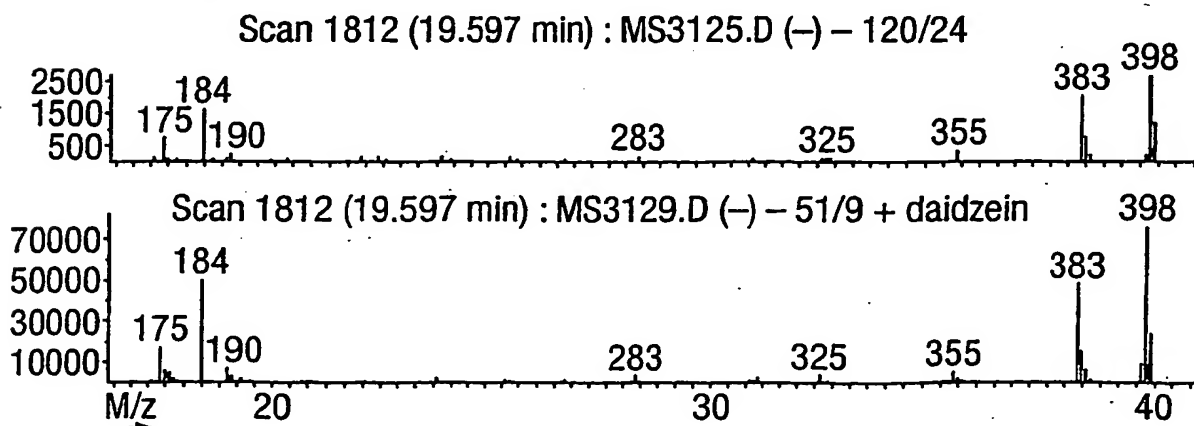


Fig.7.

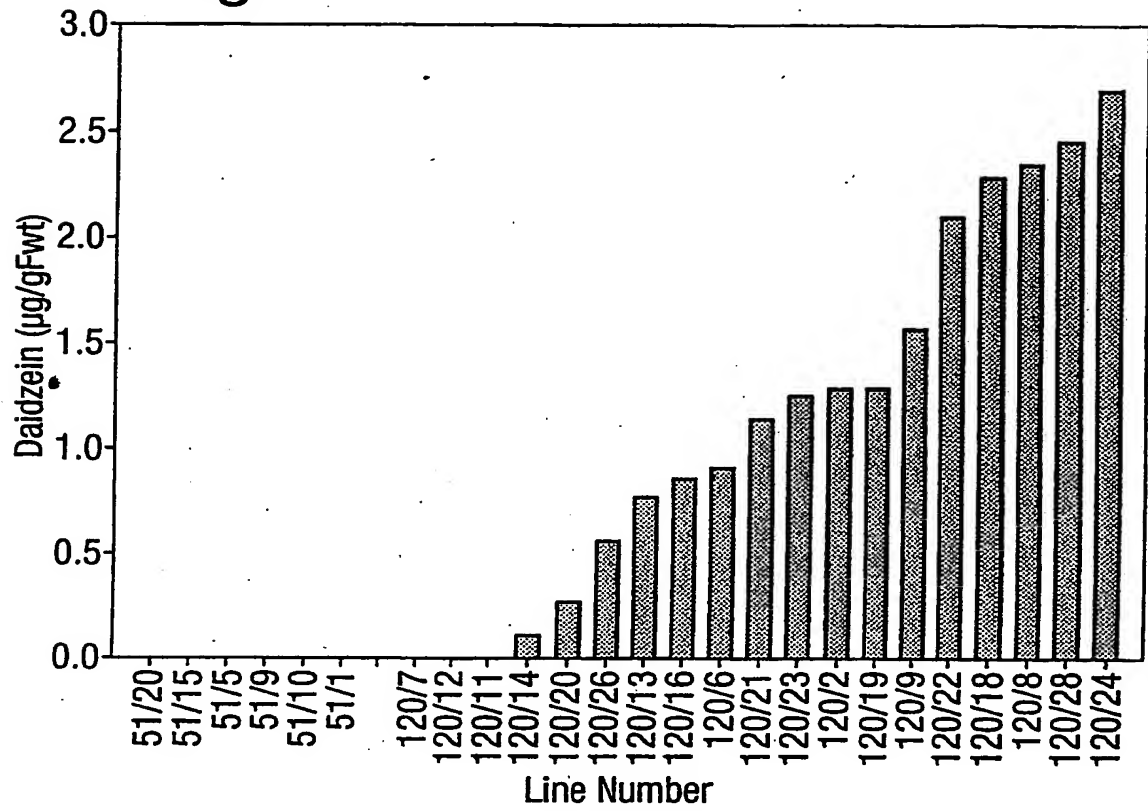


Fig.8.

